RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/537,507 A

Source: _____ IFWP

Date Processed by STIC: _____ 08/03/2006

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RAW SEQUENCE LISTING   DATE: 08/03/2006
PATENT APPLICATION: US/10/537,507A   TIME: 09:36:16

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\08032006\J537507A.raw**

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     3  <110> APPLICANT: Aarhus Universitet
     5  <120> TITLE OF INVENTION: Method for determining predisposition to manifestation of
immune system
     6        related diseases
     8  <130> FILE REFERENCE: P 706 DK 02
C--> 10  <140> CURRENT APPLICATION NUMBER: US/10/537,507A
C--> 10  <141> CURRENT FILING DATE: 2005-06-03
    10  <160> NUMBER OF SEQ ID NOS: 8
    12  <170> SOFTWARE: PatentIn version 3.1
    14  <210> SEQ ID NO: 1
    15  <211> LENGTH: 671
    16  <212> TYPE: PRT
    17  <213> ORGANISM: Homo sapiens
    19  <400> SEQUENCE: 1
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    22  1               5                   10                  15
    25  Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
    26              20                  25                  30
    29  Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
    30          35                  40                  45
    33  Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
    34      50                  55                  60
    37  Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
    38  65                  70                  75                  80
    41  Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
    42                  85                  90                  95
    45  Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
    46              100                 105                 110
    49  Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
    50          115                 120                 125
    53  Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
    54      130                 135                 140
    57  Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
    58  145                 150                 155                 160
    61  Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
    62                  165                 170                 175
    65  Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
    66              180                 185                 190
    69  Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
    70              195                 200                 205
    73  Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
    74      210                 215                 220
    77  Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
    78  225                 230                 235                 240
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 81 Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
 82             245             250             255
 85 Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
 86             260             265             270
 89 Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
 90         275             280             285
 93 Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
 94     290             295             300
 97 Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
 98 305             310             315             320
101 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
102             325             330             335
105 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
106         340             345             350
109 Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
110         355             360             365
113 Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
114     370             375             380
117 Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
118 385             390             395             400
121 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
122             405             410             415
125 Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
126             420             425             430
129 Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
130         435             440             445
133 Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
134     450             455             460
137 Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
138 465             470             475             480
141 Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
142             485             490             495
145 Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
146             500             505             510
149 Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
150         515             520             525
153 Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
154     530             535             540
157 Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
158 545             550             555             560
161 Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
162             565             570             575
165 Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
166         580             585             590
169 Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
170         595             600             605
173 Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
174     610             615             620
177 Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
```

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```
178 625               630               635               640
181 Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys
182               645               650               655
185 Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
186               660               665               670
189 <210> SEQ ID NO: 2
190 <211> LENGTH: 170
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
197 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala
198 1               5               10               15
201 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
202               20               25               30
205 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
206               35               40               45
209 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
210       50               55               60
213 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
214 65               70               75               80
217 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
218               85               90               95
221 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
222               100               105               110
225 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
226       115               120               125
229 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
230       130               135               140
233 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
234 145               150               155               160
237 Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
238               165               170
241 <210> SEQ ID NO: 3
242 <211> LENGTH: 2061
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: cDNA encoding human MASP-2
249 <400> SEQUENCE: 3
250 atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg      60
252 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc     120
254 aatgaccagg agcggcgctg gaccctgact gcaccccc+g gctaccgcct gcgcctctac     180
256 ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc     240
258 tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc     300
260 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac     360
262 tactccaacg agaagccgtt cacggggttc gaggccttct atgcagccga ggacattgac     420
264 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg     480
266 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc     540
268 tcagccctgt gctccggcca ggtcttcacc cagaggtctg gggagctcag cagccctgaa     600
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RAW SEQUENCE LISTING   DATE: 08/03/2006
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270 tacccacggc cgtatcccaa actctccagt tgcacttaca gcatcagcct ggaggagggg   660
272 ttcagtgtca ttctggactt tgtgggagtcc ttcgatgtgg agacacaccc tgaaaccctg  720
274 tgtccctacg actttctcaa gattcaaaca gacagagaag aacatggccc attctgtggg   780
276 aagacattgc cccacaggat tgaaacaaaa agcaacacgg tgaccatcac ctttgtcaca   840
278 gatgaatcag gagaccacac aggctggaag atccactaca cgagcacagc gcagccttgc   900
280 ccttatccga tggcgccacc taatggccac gtttcacctg tgcaagccaa atacatcctg   960
282 aaagacagct tctccatctt ttgcgagact ggctatgagc ttctgcaagg tcacttgccc   1020
284 ctgaaatcct ttactgcagt ttgtcagaaa gatggatctt gggaccggcc aatgcccgcg   1080
286 tgcagcattg ttgactgtgg ccctcctgat gatctaccca gtggccgagt ggagtacatc   1140
288 acaggtcctg gagtgaccac ctacaaagct gtgattcagt acagctgtga agagaccttc   1200
290 tacacaatga aagtgaatga tggtaaatat gtgtgtgagg ctgatggatt ctggacgagc   1260
292 tccaaaggag aaaaatcact cccagtctgt gagcctgttt gtggactatc agcccgcaca   1320
294 acaggagggc gtatatatgg agggcaaaag gcaaaacctg gtgattttcc ttggcaagtc   1380
296 ctgatattag gtggaaccac agcagcaggt gcacttttat atgacaactg ggtcctaaca   1440
298 gctgctcatg ccgtctatga gcaaaaacat gatgcatccg ccctggacat tcgaatgggc   1500
300 accctgaaaa gactatcacc tcattataca caagcctggt ctgaagctgt ttttatacat   1560
302 gaaggttata ctcatgatgc tggctttgac aatgacatag cactgattaa attgaataac   1620
304 aaagttgtaa tcaatagcaa catcacgcct atttgtctgc caagaaaaga agctgaatcc   1680
306 tttatgagga cagatgacat tggaactgca tctggatggg gattaaccca aaggggtttt   1740
308 cttgctagaa atctaatgta tgtcgacata ccgattgttg accatcaaaa atgtactgct   1800
310 gcatatgaaa agccacccta tccaagggga agtgtaactg ctaacatgct ttgtgctggc   1860
312 ttagaaagtg ggggcaagga cagctgcaga ggtgacagcg gaggggcact ggtgtttcta   1920
314 gatagtgaaa cagagaggtg gtttgtggga ggaatagtgt cctggggttc catgaattgt   1980
316 ggggaagcag gtcagtatgg agtctacaca aaagttatta actatattcc ctggatcgag   2040
318 aacataatta gtgattttta a                                             2061
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 558
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: cDNA encoding human MAp-19
329 <400> SEQUENCE: 4
330 atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg   60
332 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc   120
334 aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac   180
336 ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc   240
338 tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc   300
340 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac   360
342 tactccaacg agaagccgtt cacggggttc gaggccttct atgcagccga ggacattgac   420
344 gagtgccagg tggcccccggg agaggcgccc acctgcgacc accactgcca caaccacctg   480
346 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc   540
348 tcagagcaga gcctctag                                                 558
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 21
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: upper PCR primer
359 <400> SEQUENCE: 5
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RAW SEQUENCE LISTING   DATE: 08/03/2006
PATENT APPLICATION: US/10/537,507A   TIME: 09:36:16

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\08032006\J537507A.raw**

```
360 gcgagtacga cttcgtcaag g                              21
363 <210> SEQ ID NO: 6
364 <211> LENGTH: 21
365 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: lower PCR primer
371 <400> SEQUENCE: 6
372 ctcggctgca tagaaggcct c                              21
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
378 <213> ORGANISM: Artificial Sequence
380 <220> FEATURE:
381 <223> OTHER INFORMATION: upper PCR primer
383 <400> SEQUENCE: 7
384 ccagaccttt ggaaagttag c                              21
387 <210> SEQ ID NO: 8
388 <211> LENGTH: 21
389 <212> TYPE: DNA
390 <213> ORGANISM: Artificial Sequence
392 <220> FEATURE:
393 <223> OTHER INFORMATION: lower PCR primer
395 <400> SEQUENCE: 8
396 ggctcaagtt ccaagtattg c                              21
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VERIFICATION SUMMARY   DATE: 08/03/2006
PATENT APPLICATION: **US/10/537,507A**   TIME: 09:36:17

Input Set : **A:\PTO.RJ.txt**
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date